

SEQUENCE LISTING

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<110> Stewart, A. F.
      Zhang, Y.
      Hallet, B.

<120> A New Tyrosine Recombinase for Genetic Engineering

<130> 9882-012-999

<160> 10

<170> PatentIn version 3.0

<210> 1
<211> 244
<212> DNA
<213> Bacillus thuringiensis

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aatatatcat tattccttga cacatacatg ttctttttt atacaaaaaa taataacaaca      120
caatattaat tgtgttgtat taggtgttat aataaatata aatctagggg tttaacgcaa      180
cacaatttat cgataaataa atacttttag acgcaacaca attttagac gcggaggaaa      240
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<213> Bacillus thuringiensis

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cacaatatta attgtgtgtt attaggtgtt ataataaaata taaatctagg gggttaacgc      180
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1 5 10 15		
acc gag aac act gtt cag gga tac aca tca ggt att aga cag tac ata	96	
Thr Glu Asn Thr Val Gln Gly Tyr Thr Ser Gly Ile Arg Gln Tyr Ile		
20 25 30		
aaa tgg ttt gaa ggt tcc tat gac aga aaa ttg aca aaa ttg tac cga	144	
Lys Trp Phe Glu Gly Ser Tyr Asp Arg Lys Leu Thr Lys Leu Tyr Arg		
35 40 45		
caa aat atc tta gag tac att agt tat tta aag aat gtc aaa atg ttg	192	
Gln Asn Ile Leu Glu Tyr Ile Ser Tyr Leu Lys Asn Val Lys Met Leu		
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aac gcc aag tcc att aac cac aag att agt agc ctt gct aaa ttt aat	240	
Asn Ala Lys Ser Ile Asn His Lys Ile Ser Ser Leu Ala Lys Phe Asn		
65 70 75 80		
gaa ttt cta ata cag aaa gga agt caa caa gat caa gta att tta tta	288	
Glu Phe Leu Ile Gln Lys Gly Ser Gln Gln Asp Gln Val Ile Leu Leu		
85 90 95		
gat gta aaa aag ttt tta caa agt gtg tta gag gat aat aac aaa cgt	336	
Asp Val Lys Lys Phe Leu Gln Ser Val Leu Glu Asp Asn Asn Lys Arg		
100 105 110		
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Asn Tyr Ala Ile Ala Thr Leu Leu Ala Tyr Thr Gly Val Arg Ile Ser		
115 120 125		
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Glu Ala Leu Ser Ile Lys Met Asn Asp Phe Asn Leu Gln Thr Gly Glu		
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tgt att att cga agt gga aaa gga ggt aaa caa cga att gta tta cta	480	
Cys Ile Ile Arg Ser Gly Lys Gly Gly Lys Gln Arg Ile Val Leu Leu		
145 150 155 160		
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Asn Ser Lys Val Leu Ser Ala Ile Lys Asp Tyr Leu Ile Asp Arg Lys		
165 170 175		
aca tac agt aca gca cat gaa tct ccg tat ctt ttt att agt aaa aag	576	
Thr Tyr Ser Thr Ala His Glu Ser Pro Tyr Leu Phe Ile Ser Lys Lys		
180 185 190		
cga gaa aag ctc gac cgt acg gtc aat cgt atc ttt aaa tca tac	624	
Arg Glu Lys Leu Asp Arg Thr Val Val Asn Arg Ile Phe Lys Ser Tyr		
195 200 205		
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Arg Asn Val Ile Thr Pro His Gln Leu Arg His Phe Phe Cys Thr Asn		
210 215 220		
gca att caa aaa gga ttt agc att cat gaa gtt gca aat caa gct ggg	720	
Ala Ile Gln Lys Gly Phe Ser Ile His Glu Val Ala Asn Gln Ala Gly		
225 230 235 240		
cac tct aac atc cat acg aca cta ctt tac aca aat cca aac caa ctg	768	
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Lys Trp Phe Glu Gly Ser Tyr Asp Arg Lys Leu Thr Lys Leu Tyr Arg  
 35 40 45

Gln Asn Ile Leu Glu Tyr Ile Ser Tyr Leu Lys Asn Val Lys Met Leu  
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Asn Ala Lys Ser Ile Asn His Lys Ile Ser Ser Leu Ala Lys Phe Asn  
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Glu Phe Leu Ile Gln Lys Gly Ser Gln Gln Asp Gln Val Ile Leu Leu  
 85 90 95

Asp Val Lys Lys Phe Leu Gln Ser Val Leu Glu Asp Asn Asn Lys Arg  
 100 105 110

Asn Tyr Ala Ile Ala Thr Leu Leu Ala Tyr Thr Gly Val Arg Ile Ser  
 115 120 125

Glu Ala Leu Ser Ile Lys Met Asn Asp Phe Asn Leu Gln Thr Gly Glu  
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Cys Ile Ile Arg Ser Gly Lys Gly Gly Lys Gln Arg Ile Val Leu Leu  
 145 150 155 160

Asn Ser Lys Val Leu Ser Ala Ile Lys Asp Tyr Leu Ile Asp Arg Lys  
 165 170 175

Thr Tyr Ser Thr Ala His Glu Ser Pro Tyr Leu Phe Ile Ser Lys Lys  
 180 185 190

Arg Glu Lys Leu Asp Arg Thr Val Val Asn Arg Ile Phe Lys Ser Tyr  
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Arg Asn Val Ile Thr Pro His Gln Leu Arg His Phe Phe Cys Thr Asn  
 210 215 220

Ala Ile Gln Lys Gly Phe Ser Ile His Glu Val Ala Asn Gln Ala Gly  
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<223> n = a, t, g, or c

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ttta                                         124

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